

1
SEQUENCE LISTING

<110> Yu et al.

<120> Neutrokin- α and Neutrokin- α Splice Variants

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<141> 2000-02-22

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<151> 1999-03-02

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Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg
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Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu
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Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn
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Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Val Thr Gln
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Asp Cys Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys
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Gly Ser Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser
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Ala Leu Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr
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Phe Phe Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met
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Gly His Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu
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Ser Leu Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu
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Pro Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly
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Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro
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75

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Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro
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Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser
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Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly
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Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala
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Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro
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Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu
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Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu
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Gln Asp Gln Gly Gly Leu Val Thr Glu Thr Ala Asp Pro Gly Ala Gln
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Ala Gln Gln Gly Leu Gly Phe Gln Lys Leu Pro Glu Glu Glu Pro Glu
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Thr Asp Leu Ser Pro Gly Leu Pro Ala Ala His Leu Ile Gly Ala Pro
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Leu Lys Gly Gln Gly Leu Gly Trp Glu Thr Thr Lys Glu Gln Ala Phe
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Leu Thr Ser Gly Thr Gln Phe Ser Asp Ala Glu Gly Leu Ala Leu Pro
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Gly Leu Val Gln Leu Arg Arg Gly Glu Arg Val Tyr Val Asn Ile Ser
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35 40 45

Pro Pro Pro Pro Pro Leu Pro Pro Pro Pro Pro Pro Pro Leu Pro
50 55 60

Pro Leu Pro Leu Pro Pro Leu Lys Lys Arg Gly Asn His Ser Thr Gly
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Leu Cys Leu Leu Val Met Phe Phe Met Val Leu Val Ala Leu Val Gly
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Leu Gly Leu Gly Met Phe Gln Leu Phe His Leu Gln Lys Glu Leu Ala
100 105 110

Glu Leu Arg Glu Ser Thr Ser Gln Met His Thr Ala Ser Ser Leu Glu
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Lys Gln Ile Gly His Pro Ser Pro Pro Pro Glu Lys Lys Glu Leu Arg
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Lys Val Ala His Leu Thr Gly Lys Ser Asn Ser Arg Ser Met Pro Leu
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Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu Leu Ser Gly Val Lys Tyr
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Lys Lys Gly Gly Leu Val Ile Asn Glu Thr Gly Leu Tyr Phe Val Tyr
180 185 190

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195 200 205

His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro Gln Asp Leu Val Met
210 215 220

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Arg Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr Ser Ala Asp His
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 aacctcttag gaaggaagga ttcttaactg ggaaataacc caaaaaaann ttaaangggg 420
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 Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu
 35 40 45
 gct gca acc ttg ctg ctg gca ctg ctg tct tgc tgc ctc acg gtg gtg 192
 Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val
 50 55 60
 tct ttc tac cag gtg gcc gcc ctg caa ggg gac ctg gcc agc ctc cgg 240
 Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg
 65 70 75 80
 gca gag ctg cag ggc cac cac gcg gag aag ctg cca gca gga gca gga 288
 Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly

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	85	16 90	95	
gcc ccc aag gcc ggc ctg gag gaa gct cca gct gtc acc gcg gga ctg				336
Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu	100	105	110	
aaa atc ttt gaa cca cca gct cca gga gaa ggc aac tcc agt cag aac				384
Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn	115	120	125	
agc aga aat aag cgt gcc gtt cag ggt cca gaa gaa aca gga tct tac				432
Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Gly Ser Tyr	130	135	140	
aca ttt gtt cca tgg ctt ctc agc ttt aaa agg gga agt gcc cta gaa				480
Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala Leu Glu	145	150	155	160
gaa aaa gag aat aaa ata ttg gtc aaa gaa act ggt tac ttt ttt ata				528
Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr Phe Phe Ile	165	170	175	
tat ggt cag gtt tta tat act gat aag acc tac gcc atg gga cat cta				576
Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly His Leu	180	185	190	
att cag agg aag aag gtc cat gtc ttt ggg gat gaa ttg agt ctg gtg				624
Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu Val	195	200	205	
act ttg ttt cga tgt att caa aat atg cct gaa aca cta ccc aat aat				672
Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu Pro Asn Asn	210	215	220	
tcc tgc tat tca gct ggc att gca aaa ctg gaa gaa gga gat gaa ctc				720
Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly Asp Glu Leu	225	230	235	240
caa ctt gca ata cca aga gaa aat gca caa ata tca ctg gat gga gat				768
Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu Asp Gly Asp	245	250	255	
gtc aca ttt ttt ggt gca ttg aaa ctg ctg tgacctactt acaccatgtc				818
Val Thr Phe Phe Gly Ala Leu Lys Leu Leu	260	265		
tgtagctatt ttctccctt tctctgtacc tctaagaaga aagaatctaa ctgaaaatac				878
caaaaaaaaaa aaaaaaaaaa aaaaaa				903

<210> 19
 <211> 266
 <212> PRT
 <213> Homo sapiens

<400> 19
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Lys Lys Arg Glu Glu Met Lys Leu Lys Glu Cys Val Ser Ile Leu Pro
20 25 30

Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu
35 40 45

Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val
50 55 60

Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg
65 70 75 80

Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly
85 90 95

Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu
100 105 110

Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn
115 120 125

Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Gly Ser Tyr
130 135 140

Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala Leu Glu
145 150 155 160

Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr Phe Phe Ile
165 170 175

Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly His Leu
180 185 190

Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu Val
195 200 205

Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu Pro Asn Asn
210 215 220

Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly Asp Glu Leu
225 230 235 240

Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu Asp Gly Asp
245 250 255

Val Thr Phe Phe Gly Ala Leu Lys Leu Leu
260 265

<210> 20

<211> 136

<212> PRT

<213> Homo sapiens

<400> 20

His Ser Val Leu His Leu Val Pro Ile Asn Ala Thr Ser Lys Asp Asp
1 5 10 15

Ser Asp Val Thr Glu Val Met Trp Gln Pro Ala Leu Arg Arg Gly Arg

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Gly Leu Gln Ala Gln Gly Tyr Gly Val Arg Ile Gln Asp Ala Gly Val
35 40 45

Tyr Leu Leu Tyr Ser Gln Val Leu Phe Gln Asp Val Thr Phe Thr Met
50 55 60

Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg Gln Glu Thr Leu Phe
65 70 75 80

Arg Cys Ile Arg Ser Met Pro Ser His Pro Asp Arg Ala Tyr Asn Ser
85 90 95

Cys Tyr Ser Ala Gly Val Phe His Leu His Gln Gly Asp Ile Leu Ser
100 105 110

Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser Pro His Gly
115 120 125

Thr Phe Leu Gly Phe Val Lys Leu
130 135

<210> 21

<211> 462

<212> DNA

<213> Homo sapiens

<400> 21

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tctgaaactc cgaccatcca gaaagggttct tacacctttg ttccttggct gctttctttc 120
aaacgtgggt ctgccctgga agagaaagaa aacaaaatcc tggttaaaga aactgggttac 180
ttctttatct acggtcaggt tctttacact gataagacct acgccatggg tcacctgatt 240
cagcgtaaga aagttcacgt tttcggtgac gagctgtctc tggttactct gtttcgctgc 300
attcagaaca tgccggaac tcttctaac aactcctgct actctgctgg catcgcaaaa 360
ctggaagagg gtgatgaact gcagctggca attcctcgtg aaaacgcaca aatttctctg 420
gacggtgatg taaccttctt tgggtgcactg aaacttctgt aa 462

<210> 22

<211> 1040

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(468)

<400> 22

cgc gtg gta gac ctc tca gct cct cct gca cca tgc ctg cct gga tgc 48
Arg Val Val Asp Leu Ser Ala Pro Pro Ala Pro Cys Leu Pro Gly Cys
1 5 10 15

cgc cat tct caa cat gat gat aat gga atg aac ctc aga aac aga act 96
Arg His Ser Gln His Asp Asp Asn Gly Met Asn Leu Arg Asn Arg Thr
20 25 30

tac aca ttt gtt cca tgg ctt ctc agc ttt aaa aga gga aat gcc ttg 144
Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Asn Ala Leu

00589287.050800

35

40

45

gag gag aaa gag aac aaa ata gtg gtg agg caa aca ggc tat ttc ttc 192
 Glu Glu Lys Glu Asn Lys Ile Val Val Arg Gln Thr Gly Tyr Phe Phe
 50 55 60

atc tac agc cag gtt cta tac acg gac ccc atc ttt gct atg ggt cat 240
 Ile Tyr Ser Gln Val Leu Tyr Thr Asp Pro Ile Phe Ala Met Gly His
 65 70 75 80

gtc atc cag agg aag aaa gta cac gtc ttt ggg gac gag ctg agc ctg 288
 Val Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu
 85 90 95

gtg acc ctg ttc cga tgt att cag aat atg ccc aaa aca ctg ccc aac 336
 Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Lys Thr Leu Pro Asn
 100 105 110

aat tcc tgc tac tcg gct ggc atc gcg agg ctg gaa gaa gga gat gag 384
 Asn Ser Cys Tyr Ser Ala Gly Ile Ala Arg Leu Glu Glu Gly Asp Glu
 115 120 125

att cag ctt gca att cct cgg gag aat gca cag att tca cgc aac gga 432
 Ile Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Arg Asn Gly
 130 135 140

gac gac acc ttc ttt ggt gcc cta aaa ctg ctg taa ctcacttgct 478
 Asp Asp Thr Phe Phe Gly Ala Leu Lys Leu Leu
 145 150 155

ggagtgcgtg atcccccttcc ctcgctttct ctgtacctcc gagggagaaa cagacgactg 538

gaaaaactaa aagatgggga aagccgtcag cgaaagtttt ctcgtagacc gttgaatctg 598

atccaaacca ggaaatataa cagacagcca caaccgaagt gtgccatgtg agttatgaga 658

aacggagccc gcgctcagaa agaccggatg aggaagaccg ttttctccag tcctttgcca 718

acacgcaccg caaccttgct ttttgcttg ggtgacacat gttcagaatg cagggagatt 778

tccttggtttt gcgatttgcc atgagaagag ggcccacaac tgcaggtcac tgaagcattc 838

acgctaagtc tcaggattta ctctcccttc tcatgctaag tacacacacg ctcttttcca 898

ggtaatacta tgggatacta tggaaagggt gtttggtttt aaatctagaa gtcttgaact 958

ggcaatagac aaaaatcctt ataaattcaa gtgtaaaata aacttaatta aaaagggtta 1018

agtggtgaaaa aaaaaaaaaa aa 1040

<210> 23

<211> 155

<212> PRT

<213> Homo sapiens

<400> 23

Arg Val Val Asp Leu Ser Ala Pro Pro Ala Pro Cys Leu Pro Gly Cys

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1 5 10 15
 Arg His Ser Gln His Asp Asp Asn Gly Met Asn Leu Arg Asn Arg Thr
 20 25 30
 Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Asn Ala Leu
 35 40 45
 Glu Glu Lys Glu Asn Lys Ile Val Val Arg Gln Thr Gly Tyr Phe Phe
 50 55 60
 Ile Tyr Ser Gln Val Leu Tyr Thr Asp Pro Ile Phe Ala Met Gly His
 65 70 75 80
 Val Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu
 85 90 95
 Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Lys Thr Leu Pro Asn
 100 105 110
 Asn Ser Cys Tyr Ser Ala Gly Ile Ala Arg Leu Glu Glu Gly Asp Glu
 115 120 125
 Ile Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Arg Asn Gly
 130 135 140
 Asp Asp Thr Phe Phe Gly Ala Leu Lys Leu Leu
 145 150 155

<210> 24
 <211> 26
 <212> DNA
 <213> Homo sapiens

<400> 24
 ccaccagctc caggagaagg caactc

26

<210> 25
 <211> 19
 <212> DNA
 <213> Homo sapiens

<400> 25
 accgcgggac tgaaaatct

19

<210> 26
 <211> 23
 <212> DNA
 <213> Homo sapiens

<400> 26
 cacgcttatt tctgctgttc tga

23

<210> 27
 <211> 657
 <212> DNA
 <213> Homo sapiens

<400> 27
 taccaggtgg cggccgtgca aggggacctg gccagcctcc gggcagagct gcagggccac 60
 cagcgggaga agctgccagc aagagcaaga gcccacaagg ccggtctggg ggaagctcca 120
 gctgtcaccg caggactgaa aatctttgaa ccaccagctc caggagaagg caactccagt 180
 cagagcagca gaaataagcg tgctattcag ggtgcagaag aaacagtcac tcaagactgc 240
 ttgcaactga ttgcagacag tgaaacacca actatacaaa aaggatctta cacatttgtt 300

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ccatggcttc tcagctttaa aaggggaagt gccctagaag aaaaagagaa taaaatattg 360
 gtcaaagaaa ctggttactt ttttatatat ggtcagggtt tatacactga taagacctat 420
 gccatgggac atctaattca gaggaaaaaa gtccatgtct ttggggatga attgagtctg 480
 gtgactttgt ttcgatgtat tcaaaatatg cctgaaacac taccataa ttcctgctat 540
 tcagctggca ttgcaaaact ggaagaagga gatgaacttc aacttgcaat accacgagaa 600
 aatgcacaaa tatcactgga tggagatgtc acattttttg gtgcctcaa actgctg 657

<210> 28

<211> 219

<212> PRT

<213> Homo sapiens

<400> 28

Tyr Gln Val Ala Ala Val Gln Gly Asp Leu Ala Ser Leu Arg Ala Glu
 1 5 10 15

Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Arg Ala Arg Ala Pro
 20 25 30

Lys Ala Gly Leu Gly Glu Ala Pro Ala Val Thr Ala Gly Leu Lys Ile
 35 40 45

Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Ser Ser Arg
 50 55 60

Asn Lys Arg Ala Ile Gln Gly Ala Glu Glu Thr Val Ile Gln Asp Cys
 65 70 75 80

Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys Gly Ser
 85 90 95

Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala Leu
 100 105 110

Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr Phe Phe
 115 120 125

Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly His
 130 135 140

Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu
 145 150 155 160

Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu Pro Asn
 165 170 175

Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly Asp Glu
 180 185 190

Leu Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu Asp Gly
 195 200 205

Asp Val Thr Phe Phe Gly Ala Leu Lys Leu Leu
 210 215

<210> 29

<211> 657

<212> DNA

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<213> Homo sapiens

<400> 29

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gctgtcaccg cgggactgaa aatctttgaa ccaccagctc caggagaagg caactccagt 180
cagagcagca gaaataagcg tgctattcag ggtgcagaag aaacagtcac tcaagactgc 240
ttgcaactga ttgcagacag tgaaacacca actatacaaa aaggatctta cacatttgtt 300
ccatggcttc tcagctttaa aaggggaagt gccctagaag aaaaagagaa taaaatattg 360
gtcaaagaaa ctggttactt ttttatatat ggtcagggtt tatacactga taagacctat 420
gccatgggac atctaattca gaggaaaaaa gtccatgtct ttggggatga attgagtctg 480
gtgactttgt ttcatgtat tcaaaatatg cctgaaacac taccataaa ttctgtctat 540
tcagctggca ttgcaaaact ggaagaaggg gatgaacttc aacttgcaat accacgagaa 600
aatgcacaaa tatcactgga tggagatgtc acattttttg gtgccctcaa actgctg 657

<210> 30

<211> 219

<212> PRT

<213> Homo sapiens

<400> 30

Tyr Gln Val Ala Ala Val Gln Gly Asp Leu Ala Ser Leu Arg Ala Glu
1 5 10 15
Leu Gln Ser His His Ala Glu Lys Leu Pro Ala Arg Ala Arg Ala Pro
20 25 30
Lys Ala Gly Leu Gly Glu Ala Pro Ala Val Thr Ala Gly Leu Lys Ile
35 40 45
Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Ser Ser Arg
50 55 60
Asn Lys Arg Ala Ile Gln Gly Ala Glu Glu Thr Val Ile Gln Asp Cys
65 70 75 80
Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys Gly Ser
85 90 95
Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala Leu
100 105 110
Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr Phe Phe
115 120 125
Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly His
130 135 140
Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu
145 150 155 160
Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu Pro Asn
165 170 175
Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly Asp Glu
180 185 190
Leu Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu Asp Gly
195 200 205

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Asp Val Thr Phe Phe Gly Ala Leu Lys Leu Leu
 210 215

<210> 31
 <211> 38
 <212> DNA
 <213> Homo sapiens

<400> 31
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38

<210> 32
 <211> 49
 <212> DNA
 <213> Homo sapiens

<400> 32
 ctgggttcggc ccaaggtacc aagcttgtagc cttagatctt ttctagatc

49

<210> 33
 <211> 21
 <212> DNA
 <213> Homo sapiens

<400> 33
 ctggtagttc ttcggagtgt g

21

<210> 34
 <211> 19
 <212> DNA
 <213> Homo sapiens

<400> 34
 cgcgtagaa acggcgacc

19

<210> 35
 <211> 22
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (7)
 <223> n equals deoxyinosine

<220>
 <221> misc_feature
 <222> (12)
 <223> n equals deoxyinosine

<220>
 <221> misc_feature
 <222> (16)
 <223> n equals deoxyinosine

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<400> 35
taccagntgg cngccntgca ag

22

<210> 36
<211> 22
<212> DNA
<213> Homo sapiens

<220>
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<222> (3)
<223> n equals deoxyinosine

<220>
<221> misc_feature
<222> (14)
<223> n equals deoxyinosine

<220>
<221> misc_feature
<222> (16)..(17)
<223> n equals deoxyinosine

<400> 36
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22

<210> 37
<211> 866
<212> DNA
<213> Mus musculus

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gaagatatga aagtgggata tgatcccatc actccgcaga aggaggaggg tgccctggttt 120
gggatctgca gggatggaag gctgctggct gctaccctcc tgctggccct gttgtccagc 180
agtttcacag cgatgtcctt gtaccagttg gctgccttgc aagcagacct gatgaacctg 240
cgcattggagc tgcagagcta ccgaggttca gcaacaccag ccgccgcggg tgctccagag 300
ttgaccgctg gagtcaaact cctgacaccg gcagctcctc gacccccaaa ctccagccgc 360
ggccacagga acagacgcgc cttccaggga ccagaggaaa cagaacaaga tgtagacctc 420
tcagctcctc ctgcaccatg cctgcctgga tgccgccatt ctcaacatga tgataatgga 480
atgaacctca gaaacatcat tcaagactgt ctgcagctga ttgcagacag cgacacgccg 540
gccttggagg agaaagagaa caaaatagtg gtgaggcaaa caggctattt cttcatctac 600
agccagggtc tatacacgga ccccatcttt gctatgggtc atgtcatcca gaggaagaaa 660
gtacacgtct ttggggacga gctgagcctg gtgaccctgt tccgatgtat tcagaatatg 720
cccaaaacac tgccaacaa ttctgctac tcggctggca tcgcgaggct ggaagaagga 780
gatgagattc agcttgcaat tctcggggag aatgcacaga tttcacgcaa cggagacgac 840
accttctttg gtgcctaaa actgct 866

<210> 38
<211> 177
<212> PRT
<213> Mus musculus

<400> 38
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1 5 10 15

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25

Gly Tyr Asp Thr Lys Gly Ala Trp Gly Cys Arg Asp Gly Arg Ala Ala
20 25 30

Thr Ala Ser Ser Ser Thr Ala Met Ser Tyr Ala Ala Ala Asp Met Asn
35 40 45

Arg Met Ser Tyr Arg Gly Ser Ala Thr Ala Ala Ala Gly Ala Thr Ala
50 55 60

Gly Val Lys Thr Ala Ala Arg His Asn Ser Ser Arg Gly His Arg Asn
65 70 75 80

Arg Arg Ala Gly Thr Asp Val Asp Ser Ala Ala Cys Gly Cys Arg His
85 90 95

Ser His Asp Asp Asn Gly Met Asn Arg Asn Asp Cys Ala Asp Ser Asp
100 105 110

Thr Ala Lys Asn Lys Val Val Arg Thr Gly Tyr Tyr Ser Val Tyr Thr
115 120 125

Asp Ala Met Gly His Val Arg Lys Lys Val His Val Gly Asp Ser Val
130 135 140

Thr Arg Cys Asn Met Lys Thr Asn Asn Ser Cys Tyr Ser Ala Gly Ala
145 150 155 160

Arg Gly Asp Ala Arg Asn Ala Ser Arg Asn Gly Asp Asp Thr Gly Ala
165 170 175

Lys

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